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(54) **Nucleic acid probes to mycobacterium tuberculosis.**

(57) Hybridization assay probes specific for members of the Mycobacterium tuberculosis Complex and no other Mycobacterium species.

Keywords: Hybridization probes Mycobacterium tuberculosis complex specific ...

EP 0 572 120 A1

Field of the Invention

The inventions described and claimed herein relate to the design and construction of nucleic acid probes for Mycobacterium tuberculosis Complex (TB Complex) which are capable of detecting the organisms in test samples for, e.g., sputum, urine, blood and tissue sections, food, soil and water.

Background of the Invention

Two single strands of deoxyribo- ("DNA") or ribo-("RNA") nucleic acid, formed from nucleotides (including the bases adenine (A), cytosine (C), thymidine (T), guanine (G), uracil (U), or inosine (I)), may associate ("hybridize") to form a double stranded structure in which the two strands are held together by hydrogen bonds between pairs of complementary bases. Generally, A is hydrogen bonded to T or U, while G is hydrogen bonded to C. At any point along the chain, therefore, one may find the classical base pairs AT or AU, TA or UA, GC, or CG. One may also find AG, GU and other "wobble" or mismatched base pairs.

When a first single strand of nucleic acid contains sufficient contiguous complementary bases to a second, and those two strands are brought together under conditions which will promote their hybridization, double stranded nucleic acid will result. Under appropriate conditions, DNA/DNA, RNA/DNA, or RNA/RNA hybrids may be formed.

A probe is generally a single stranded nucleic acid sequence which is complementary to some degree to a nucleic acid sequence sought to be detected ("target sequence"). It may be labelled with a detectable moiety such as a radioisotope, antigen or chemiluminescent moiety. A background description of the use of nucleic acid hybridization as a procedure for the detection of particular nucleic acid sequences is described by Kohne, U.S. Patent No. 4,851,330, and Hogan et al., EPO Patent Application No. PCT/US87/03009, entitled "Nucleic Acid Probes for Detection and/Or Quantitation of Non-Viral Organisms."

Hogan et al., supra, also describes methods for determining the presence of RNA-containing organisms in a sample which might contain such organisms. These methods require probes sufficiently complementary to hybridize to the ribosomal RNA (rRNA) of one or more non-viral organisms or groups of non-viral organisms. The mixture is then incubated under specified hybridization conditions, and assayed for hybridization of the probe and any test sample rRNA.

Hogan et al. also describes probes which detect only specifically targeted rRNA subunit subsequences in particular organisms or groups of organisms in a sample, even in the presence of many non-related organisms, or in the presence of the closest known phylogenetic neighbors. Specific examples of hybridization assay probes are provided for Mycobacterium tuberculosis. Such probe sequences do not cross react with nucleic acids from other bacterial species or infectious agent, under appropriate hybridization stringency conditions.

Summary of the Invention

This invention discloses and claims novel probes for the detection of Mycobacterium tuberculosis (TB) Complex. These probes are capable of distinguishing between the Mycobacterium tuberculosis Complex and its known closest phylogenetic neighbors. The Mycobacterium tuberculosis Complex consists of the following species: M. tuberculosis, M. bovis, M. bovis BCG, M. africanum, M. microti. These probes detect unique rRNA and gene sequences encoding rRNA, and may be used in an assay for the detection and/or quantitation of Mycobacterium tuberculosis Complex.

Organisms of the TB Complex are responsible for significant morbidity and mortality in humans. M. tuberculosis is the most common TB Complex pathogen isolated from humans. M. bovis BCG may be transmitted from infected animals to humans. M. africanum causes pulmonary tuberculosis in tropical Africa and M. microti primarily infects animals.

Tuberculosis is highly contagious, therefore rapid diagnosis of the disease is important. For most clinical laboratories assignment of an isolate to the TB Complex is sufficient because the probability that an isolate is a species other than M. tuberculosis is extremely small. A number of biochemical tests are recommended to speciate members of the TB Complex if further differentiation is required.

Classical methods for identification of mycobacteria rely on staining specimens for acid fast bacilli followed by culture and biochemical testing. It could take as long as two months to speciate an isolate using these standard methods. The use of DNA probes of this invention identifies TB Complex isolated from culture in less than an hour.

Thus, in a first aspect, the invention features a hybridization assay probe able to distinguish Mycobacterium tuberculosis from other Mycobacterium species; specifically, the probe is an oligonucleotide which hybridizes to the rRNA of the species Mycobacterium tuberculosis at a location corresponding to 23 bases in the insert

region beginning at the equivalent of base 270 of E. coli 23S rRNA, or to 21 bases in the insert region beginning at the equivalent of base 1415 of E. coli 23S rRNA, or an oligonucleotide complementary thereto; that is, the oligonucleotide comprises, consists essentially of, or consists of the sequence (SEQ ID NO: 1) GGTAGCGCTGAGACATATCCTCC, or (SEQ ID NO: 2) CAGAACTCCACACCCCCGAAG, or oligonucleotides complementary thereto, with or without a helper probe, as described below.

By "consists essentially of" is meant that the probe is provided as a purified nucleic acid which hybridizes under stringent hybridizing conditions with the desired organism and not with other related organisms. Such a probe may be linked to other nucleic acids which do not affect such hybridization. Generally, it is preferred that the probe be of between 15 and 100 (most preferably between 20 and 50) bases in size. It may, however, be provided in a vector.

In related aspects, the invention features a nucleotide polymer able to hybridize to the above oligonucleotides, a nucleic acid hybrid formed with the above oligonucleotides, and a nucleic acid sequence substantially complementary thereto. Such hybrids are useful since they allow specific detection of the TB complex organisms.

The probes of this invention offer a rapid, non-subjective method of identification and quantitation of a bacterial colony for the presence of specific rRNA sequences unique to all species and strains of Mycobacterium tuberculosis Complex.

Other features and advantages of the invention will be apparent from the following description of the preferred embodiments thereof, and from the claims.

Description of the Preferred Embodiments Probes

We have discovered DNA probes complementary to a particular rRNA sequence obtained from Mycobacterium tuberculosis. Furthermore, we have successfully used those probes in a specific assay for the detection of Mycobacterium tuberculosis, distinguishing members of the M. tuberculosis complex from their known and presumably most closely related taxonomic or phylogenetic neighbors.

We have identified suitable variable regions of the target nucleic acid by comparative analysis of rRNA sequences both published in the literature and sequences which we have determined. Computers and computer programs which may be used or adapted for the purposes herein disclosed are commercially available. Since the sequence evolution at each of the variable regions (for example, spanning a minimum of 10 nucleotides) is, for the most part, divergent, not convergent, we can confidently design probes based on a few rRNA sequences which differ between the target organism and its phylogenetically closest relatives. We have seen sufficient variation between the target organism and the closest phylogenetic relative found in the same sample to design the probe of interest.

We have identified the following useful guidelines for designing probes with desired characteristics. Because the extent and specificity of hybridization reactions such as those described herein are affected by a number of factors, manipulation of one or more of those factors will determine the exact sensitivity and specificity of a particular probe, whether perfectly complementary to its target or not. The importance and effect of various assay conditions, explained further herein, are known to those skilled in the art.

First, the stability of the probe:target nucleic acid hybrid should be chosen to be compatible with the assay conditions. This may be accomplished by avoiding long A and T rich sequences, by terminating the hybrids with G:C base pairs, and by designing the probe with an appropriate Tm. The beginning and end points of the probe should be chosen so that the length and %G and %C result in a Tm about 2-10°C higher than the temperature at which the final assay will be performed. The base composition of the probe is significant because G-C base pairs exhibit greater thermal stability as compared to A-T base pairs due to additional hydrogen bonding. Thus, hybridization involving complementary nucleic acids of higher G-C content will be stable at higher temperatures.

Conditions such as ionic strength and incubation temperature under which a probe will be used should also be taken into account in constructing a probe. It is known that hybridization will increase as the ionic strength of the reaction mixture increases, and that the thermal stability of hybrids will increase with increasing ionic strength. On the other hand, chemical reagents, such as formamide, urea, DMSO and alcohols, which disrupt hydrogen bonds, will increase the stringency of hybridization. Destabilization of the hydrogen bonds by such reagents can greatly reduce the Tm. In general, optimal hybridization for synthetic oligonucleotide probes of about 10-50 bases in length occurs approximately 5°C below the melting temperature for a given duplex. Incubation at temperatures below the optimum may allow mismatched base sequences to hybridize and can therefore result in reduced specificity.

It is desirable to have probes which hybridize only under conditions of high stringency. Under high stringency conditions only highly complementary nucleic acid hybrids will form (i.e., those having at least about 14

out of 17 bases in a contiguous series of bases being complementary); hybrids without a sufficient degree of complementarity will not form. Accordingly, the stringency of the assay conditions determines the amount of complementarity needed between two nucleic acid strands forming a hybrid. Stringency is chosen to maximize the difference in stability between the hybrid formed with the target and the nontarget nucleic acid.

Second, probes should be positioned so as to minimize the stability of the probe:nontarget nucleic acid hybrid. This may be accomplished by minimizing the length of perfect complementarity to non-target organisms, avoiding G and C rich regions of homology to non-target sequences, and by positioning the probe to span as many destabilizing mismatches as possible. Whether a probe sequence is useful to detect only a specific type of organism depends largely on the thermal stability difference between probe:target hybrids and probe:nontarget hybrids. In designing probes, the differences in these Tm values should be as large as possible (e.g., at least 2°C and preferably 5°C).

The length of the target nucleic acid sequence and, accordingly, the length of the probe sequence can also be important. In some cases, there may be several sequences from a particular region, varying in location and length, which will yield probes with the desired hybridization characteristics. In other cases, one sequence may be significantly better than another which differs merely by a single base. While it is possible for nucleic acids that are not perfectly complementary to hybridize, the longest stretch of perfectly homologous base sequence will normally primarily determine hybrid stability. While oligonucleotide probes of different lengths and base composition may be used, oligonucleotide probes preferred in this invention are between about 10 to 50 bases in length and are sufficiently homologous to the target nucleic acid.

Third, regions of the rRNA which are known to form strong internal structures inhibitory to hybridization are less preferred. Likewise, probes with extensive self-complementarity should be avoided.

As explained above, hybridization is the association of two single strands of complementary nucleic acid to form a hydrogen bonded double strand. It is implicit that if one of the two strands is wholly or partially involved in a hybrid that it will be less able to participate in formation of a new hybrid. In the case of rRNA, the molecule is known to form very stable intra-molecular hybrids. By designing a probe so that a substantial portion of the sequence of interest is single stranded, the rate and extent of hybridization may be greatly increased. If the target is the genomic sequence corresponding to the rRNA then it will naturally occur in a double stranded form, this is also the case with the product of the polymerase chain reaction (PCR). These double stranded targets are naturally inhibitory to hybridization with a probe. Finally, there can be intramolecular and intermolecular hybrids formed within a probe if there is sufficient self complementarity. Such structures can be avoided through careful probe design. Computer programs are available to search for this type of interaction.

Once a presumptive unique sequence has been identified, a complementary DNA oligonucleotide is produced. This single stranded oligonucleotide will serve as the probe in the hybridization reaction. Defined oligonucleotides may be produced by any of several well known methods, including automated solid-phase chemical synthesis using cyanoethylphosphoramidite precursors. Barone et al., 12 Nucleic Acids Research 4051, 1984. Other well-known methods for construction of synthetic oligonucleotides may, of course, be employed. Sambrook et al., 2 Molecular Cloning 11 (2d ed. 1989).

Once synthesized, selected oligonucleotide probes may also be labelled by any of several well known methods. Sambrook et al., supra. Useful labels include radio-isotopes as well as non-radioactive reporting groups. Isotopic labels include ^{3}H, ^{35}S, ^{32}P, ^{125}I, Cobalt and ^{14}C. Most methods of isotopic labelling involve the use of enzymes and include the known methods of nick translation, end labelling, second strand synthesis, and reverse transcription. When using radio-labelled probes, hybridization can be detected by autoradiography, scintillation counting, or gamma counting. The detection method selected will depend upon the hybridization conditions and the particular radio-isotope used for labelling.

Non-isotopic materials can also be used for labelling, and may be introduced internally into the sequence or at the end of the sequence. Modified nucleotides may be incorporated enzymatically or chemically and chemical modifications of the probe may be performed during or after synthesis of the probe, for example, by the use of non-nucleotide linker groups. Non-isotopic labels include fluorescent molecules, chemiluminescent molecules, enzymes, cofactors, enzyme substrates, haptens or other ligands. We currently prefer to use acridinium esters.

Following synthesis and purification of a particular oligonucleotide sequence, several procedures may be utilized to determine the acceptability of the final product. The first is polyacrylamide gel electrophoresis, which is used to determine size. Sambrook et al., supra. Such procedures are known in the art. In addition to polyacrylamide gel electrophoresis, High Pressure Liquid Chromatography ("HPLC") procedures also may be used to determine the size and purity of the oligonucleotide product. These procedures are also known to those skilled in the art.

It will be appreciated by those skilled in the art that factors which affect the thermal stability can affect probe specificity and therefore, must be controlled. Thus, the melting profile, including the melting temperature

(Tm) of the oligonucleotide/target hybrids should be determined. The preferred method is described in Arnold et al., PCT/US88/03195, filed September 21, 1988, entitled "Homogeneous Protection Assay," hereby incorporated by reference herein.

For Tm measurement using a Hybridization Protection Assay (HPA) the following technique is used. A probe:target hybrid is formed in target excess in a lithium succinate buffered solution containing lithium lauryl sulfate. Aliquots of this hybrid are diluted in the hybridization buffer and incubated for five minutes at various temperatures starting below that of the anticipated Tm (typically 55°C) and increasing in 2-5 degree increments. This solution is then diluted with a mildly alkaline borate buffer and incubated at a lower temperature (for example 50°C) for ten minutes. Under these conditions the acridinium ester attached to a single stranded probe is hydrolyzed while that attached to hybridized probe is relatively protected from hydrolysis. The amount of chemiluminescence remaining is proportional to the amount of hybrid, and is measured in a luminometer by addition of hydrogen peroxide followed by alkali. The data is plotted as percent of maximum signal (usually from the lowest temperature) versus temperature. The Tm is defined as the point at which 50% of the maximum signal remains.

In addition to the above method, oligonucleotide/target hybrid melting temperature may also be determined by isotopic methods well known to those skilled in the art. It should be noted that the Tm for a given hybrid will vary depending on the hybridization solution being used because the thermal stability depends upon the concentration of different salts, detergents, and other solutes which effect relative hybrid stability during thermal denaturation. Sambrook et al., supra.

Rate of hybridization may be measured by determining the $C_0t_{1/2}$. The rate at which a probe hybridizes to its target is a measure of the thermal stability of the target secondary structure in the probe region. The standard measurement of hybridization rate is the $C_0t_{1/2}$ which is measured as moles of nucleotide per liter times seconds. Thus, it is the concentration of probe times the half-life of hybridization at that concentration. This value is determined by hybridizing various amounts of probe to a constant amount of hybrid for a fixed time. For example, 0.05 pmol of target is incubated with 0.0012, 0.025, 0.05, 0.1 and 0.2 pmol of probe for 30 minutes. The amount of hybrid after 30 minutes is measured by HPA as described above. The signal is then plotted as a log of the percent of maximum Relative Light Units (RLU) (from the highest probe concentration) versus probe concentration (moles of nucleotide per liter). RLU are a measurement of the quantity of photons emitted by the labelled-probe measured by the luminometer. The $C_0t_{1/2}$ is found graphically from the concentration corresponding to 50% of maximum hybridization multiplied by the hybridization time in seconds. These values range from $9.0x10^{-6}$ to $9x10^{-5}$ with the preferred values being less than $3.5x10^{-5}$.

As described by Kohne and Kacian (EP 86304429.3, filed June 10, 1986), hereby incorporated by reference herein) other methods of nucleic acid reassociation can be used.

The following example sets forth synthetic probes complementary to a unique rRNA sequence, or the corresponding gene, from a target organism, Mycobacterium tuberculosis, and their use in a hybridization assay.

Example:

A probe specific for M. tuberculosis was identified by sequencing with a primer complementary to the 16S rRNA. The following sequences were characterized and shown to be specific for Mycobacterium tuberculosis; (SEQ ID NO: 1) GGTAGCGCTGAGACATATCCTCC, and (SEQ ID NO: 2) CAGAACTCCACACCCCCGAAG. Several phylogenetically near neighbors including M. kansasii, M. asiaticum and M. avium were used as comparisons with the sequence of M. tuberculosis. SEQ ID NO: 1 is 23 bases in length and hybridizes to the 23S rRNA of M. tuberculosis corresponding to bases 270-293 of E. coli. SEQ ID NO: 2 is 21 bases in length and hybridizes to the 23S rRNA of M. tuberculosis corresponding to bases 1415-1436 of E. coli.

To demonstrate the reactivity and specificity of the probe for M. tuberculosis, it was used in a hybridization assay. The probe was first synthesized with a non-nucleotide linker, then labelled with a chemiluminescent acridinium ester as described in EPO Patent Application No. PCT/US88/03361, entitled "Acridinium Ester Labeling and Purification of Nucleotide Probes filed October 5, 1988. The acridinium ester attached to unhybridized probe is rendered non-chemiluminescent under mild alkaline conditions, while the acridinium ester attached to hybridized probe is relatively resistant. Thus, it is possible to assay for hybridization of acridinium ester-labelled probe by incubation with an alkaline buffer, followed by detection of chemiluminescence in a luminometer. Results are given in RLU, the quantity of photons emitted by the labelled-probe measured by the luminometer. The conditions of hybridization, hydrolysis and detection are described in Arnold, et al., 35 Clin. Chem. 1588, 1989.

Nucleic acid hybridization was enhanced by the use of "Helper Probes" as disclosed in Hogan et al., U.S. Patent No. 5,030,557 hereby incorporated by reference herein. RNA was hybridized to the acridinium ester-labeled probe in the presence of an unlabeled Helper Probe. The probe corresponding to oligonucleotide SEQ

ID NO: 1 with helpers:

(SEQ ID NO: 3) CCGCTAACCACGACACTTTCTGTACTGCCTCTCAGCCG and

(SEQ ID NO: 4) CACAACCCCGCACACACAACCCCTACCCGGTTACCC.

The probe corresponding to oligonucleotide SEQ ID NO: 2 with helpers: (SEQ ID NO: 5)

TGATTCGTCACGGGCGCCCACACACGGGTACGGGAATATCAACCC and

(SEQ ID NO: 6) CTACTACCAGCCGAAGTTCCCACGCAGCCC and

(SEQ ID NO: 7) GGAGTTGATCGATCCGGTTTTGGGTGGTTAGTACCGC and

(SEQ ID NO: 8) GGGGTACGGGCCGTGTGTGTGCTCGCTAGAGGCTTTTCTTGGC.

In the following experiment, RNA released from one colony or >10^8 organisms was assayed. An example of such a method is provided by Murphy et al. (EP 873036412, filed April 24, 1987), hereby incorporated by reference herein. An RLU value greater than 30,000 RLU is a positive reaction; less than 30,000 is a negative reaction.

The following data show that the probes did not cross react with organisms from a wide phylogenetic cross section. The samples were also tested with a Probe (ALL BACT.) which has a very broad specificity to provide a positive control. A positive signal from this probe provides confirmation of sample adequacy.

NAME	ATCC#	RLU		
		ALL BACT.	PROBE 1	PROBE 2
Mycobacterium africanum	25420	880551	489764	589419
M. asiaticum	25276	1291076	708	1849
M. avium	25291	966107	615	1749
M. bovis	19210	1564761	1020088	717186
M. bovis BCG	35734	1532845	943131	706773
M. chelonae	14472	1581603	641	1320
M. flavescens	14474	237900	842	2001
M. fortuitum	6841	910478	641	1710
M. gastri	15754	429144	781	2416
M. gordonae	14470	1207443	749	2089
M. haemophilum	29548	709966	1090	3149
M. intracellulare	13950	277790	823	2512
M. kansasii	12478	416752	839	5688
M. malmoense	29571	149699	1176	4060
M. marinum	927	524740	699	3200
M. nonchromogenicum	19530	1541506	832	3303
M. phlei	11758	1273753	717	2286
M. scrofulaceum	19981	801447	1424	5236
M. shimoidei	27962	1609154	719	2650
M. simiae	25275	1571628	841	3152
M. smegmatis	14468	513995	789	2920
M. szulgai	35799	947710	714	2356

M. terrae	15755	480465	1492	7153
M. thermoresistibile	19527	1054152	1436	4113
M. triviale	23292	1016207	1148	4693
M. tuberculosis(avir.)	25177	1067974	767698	620393
M. tuberculosis(vir.)	27294	1543369	1012711	652815
M. ulcerans	19423	1401905	2563	5865
M. vaccae	15483	586428	729	3784
M. xenopi	19250	310648	855	3198

NAME	ATCC#	ALL BACT.	PROBE 1	PROBE 2
Acinetobacter calcoaceticus	33604	1393489	1735	9659
Actinomadura madurae	19425	572956	4388	5614
Actinomyces pyogenes	19411	1768540	1376	2527
Arthrobacter oxydans	14358	1542696	721	2126
Bacillus subtilis	6051	1441824	2424	2817
Bacteriodes fragilis	23745	1557888	843	8907
Bordetella bronchiseptica	10580	1694010	686	4113
Branhamella catarrhalis	25238	1615709	1035	7219
Brevibacterium linens	9172	904166	814	1642
Campylobacter jejuni	33560	1824094	607	3201
Candida albicans	18804	3850	763	2018
Chromobacterium violaceum	29094	1560283	993	11823
Clostridium innocuum	14501	1571465	577	2072
C. perfringens	13124	1701191	641	5757
Corynebacterium aquaticum	14665	1616486	801	1865
C. diphtheriae	11913	1464829	682	1475
C. genitalium	33030	108105	1177	1797
C. haemolyticum	9345	1512544	703	1114
C. matruchotii	33806	1871454	659	1967
C. minutissimum	23347	1024206	586	1302
C. pseudodiphtheriticum	10700	1605944	578	1155

C. pseudogenitalium	33035	497387	717	1324
C. pseudotuberculosis	19410	1730057	643	2892
C. renale	19412	1467841	544	1743
C. striatum	6940	1560152	602	1386
C. xerosis	373	1211115	651	1556
Deinococcus radiodurans	35073	1387623	644	1400
Dermatophilus congolensis	14637	1551500	810	2075
Derxia gumosa	15994	1735694	4676	4797
Erysipelothrix rhusiopathiae	19414	1623646	564	1180
Escherichia coli	10798	1685941	581	4610
Flavobacterium meniningosepticum	13253	1571895	1037	4626
Haemophilus influenzae	19418	1706963	668	2303
Klebsiella pneumoniae	23357	1692364	639	6673
Lactobacillus acidophilus	4356	226596	780	1619
Legionella pneumophila	33152	1666343	755	4184
Microbacterium lacticum	8180	620978	514	924
Mycoplasma hominis	14027	1305131	496	1410
M. pneumoniae	15531	1605424	481	1428
Neisseria meningitidis	13077	1684295	1531	8802
Nocardia asteriodes	19247	1265198	1037	1938
N. brasiliensis	19296	1483481	759	1737
N. otitidis-caviarum	14629	1462489	813	1791
Nocardiopsis dassonvillei	23218	662986	4052	4960
Oerskovia turbata	33225	1753101	591	1979
O. xanthineolytica	27402	1712806	721	1639
Paracoccus denitrificans	17741	958719	771	2910
Proteus mirabilis	25933	1761750	669	2545
Pseudomonas aeruginosa	25330	1730788	1281	6048
Rahnella aquatilis	33071	1728428	485	2884
Rhodococcus aichiensis	33611	528199	595	1169
R. aurantiacus	25936	1737076	616	2310

R. bronchialis	25592	1695267	635	1633
R. chubuensis	33609	1079495	599	1262
R. equi	6939	1762242	709	2863
R. obuensis	33610	658848	686	1482
R. sputi	29627	814617	719	1419
Staphylococcus aureus	12598	1687401	636	1434
S. epidermidis	12228	1117790	651	1255
S. mitis	9811	1807598	542	1199
S. pneumoniae	6306	1883301	532	1441
S. pyogenes	19615	1862392	728	1656
Streptomyces griseus	23345	1417914	1737	3378
Vibrio parahaemolyticus	17802	1767149	752	6429
Yersinia enterocolitica	9610	1769411	662	4255

The above data confirm that the novel probes herein disclosed and claimed are capable of distinguishing members of the Mycobacterium tuberculosis complex from their known nearest phylogenetic neighbors.

Other embodiments are within the following claims.

(1) GENERAL INFORMATION:

(i) APPLICANT: GEN-PROBE INCORPORATED
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(ii) TITLE OF INVENTION: NUCLEIC ACID PROBES TO MYCOBACTERIUM TUBERCULOSIS

(iii) NUMBER OF SEQUENCES: 8

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	23
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(ii) SEQUENCE DESCRIPTION : SEQ ID NO: 1:

GGTAGCGCTG AGACATATCC TCC 23

(3) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	21
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(ii) SEQUENCE DESCRIPTION : SEQ ID NO: 2:

CAGAACTCCA CACCCCCGAA G 21

(4) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	38
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(ii) SEQUENCE DESCRIPTION : SEQ ID NO: 3:

CCGCTAACCA CGACACTTTC TGTACTGCCT CTCAGCCG 38

(5) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION : SEQ ID NO: 4:

CACAACCCCG CACACACAAC CCCTACCCGG TTACCC 36

(6) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION : SEQ ID NO: 5:

TGATTCGTCA CGGGCGCCCA CACACGGGTA CGGGAATATC AACCC 45

(7) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION : SEQ ID NO: 6:

CTACTACCAG CCGAAGTTCC CACGCAGCCC 30

(8) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION : SEQ ID NO: 7:

GGAGTTGATC GATCCGGTTT TGGGTGGTTA GTACCGC 37

(9) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) SEQUENCE DESCRIPTION : SEQ ID NO: 8:

GGGGTACGGG CCGTGTGTGT GCTCGCTAGA GGCTTTTCTT GGC 43

Claims

1. An oligonucleotide consisting essentially of the sequence GGTAGCGCTGAGACATATCCTCC, or an oligonucleotide complementary thereto.

2. An oligonucleotide consisting essentially of the sequence CAGAACTCCACACCCCCGAAG, or an oligonucleotide complementary thereto.

3. A nucleic acid hybrid formed between an oligonucleotide of claim 1 and a nucleic acid sequence complementary to said oligonucleotide.

4. A nucleic acid hybrid formed between an oligonucleotide of claim 2 and a nucleic acid sequence complementary to said oligonucleotide.

5. A probe mix comprising the oligonucleotide of claim 1 and a helper probe.

6. A probe mix comprising the oligonucleotide of claim 2 and a helper probe.

7. The probe mix of claim 5, wherein said helper probe is an oligonucleotide comprising the oligonucleotide sequence shown as SEQ ID NOS: 3 or 4 or a complementary sequence thereto.

8. The probe mix of claim 6, wherein said helper probe is an oligonucleotide comprising the oligonucleotide sequence shown as SEQ ID NOS: 5, 6, 7 or 8 or a complementary sequence thereto.

European Patent Office

EUROPEAN SEARCH REPORT

Application Number

EP 93 30 3291

DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document with indication, where appropriate, of relevant passages	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int. Cl.5)
D,X Y	EP-A-0 272 009 (HOGEN, J. ET AL) * page 18, line 31 - page 29, line 40 *	1-4 5-6	C12Q1/68 C07H21/04
D,Y	EP-A-0 318 245 (M.L. TECHNOLOGY VENTURES L.P.) * the whole document *	5,6	
A	EP-A-0 398 677 (PRESIDENT AND FELLOWS OF HARVARD UNIV.)		
A	INTERNATIONAL JOURNAL OF SYSTEMATIC BACTERIOLOGY vol. 40, no. 4, October 1990, WASHINGTON D. C. pages 323 - 330 ROGALL, T. ET AL. 'towards a phylogeny and definition of species at the molecular level within the genus mycobacterium' * the whole document *	1-4	

TECHNICAL FIELDS SEARCHED (Int. Cl.5)

C12Q

The present search report has been drawn up for all claims

Place of search	Date of completion of the search	Examiner
THE HAGUE	15 JULY 1993	OSBORNE H.H.

CATEGORY OF CITED DOCUMENTS

X : particularly relevant if taken alone
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